

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 21, 2002, 17:08:31; Search time 16.6154 Seconds
(Without alignments)
209.686 Million cell updates/sec

Title: US-09-231-422d-2

Perfect score: 426
Sequence: 1 SVSEIQMLNHLGKHLNSMR.....KSLGEADKADVNVLTAKSQ 84

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476328 residues

:1 number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	426	100.0	115	1	PTHY_HUMAN
2	419	98.4	115	1	PTH_MACEA
3	375	88.0	115	1	PTHY_CANFA
4	365	85.7	115	1	PTHY_BOVIN
5	364	85.4	115	1	PTHY_PIG
6	317	74.4	115	1	PTHY_RAT
7	183.5	43.1	119	1	PTHY_CHICK
8	74.5	17.5	824	1	SVL_THEMEA
9	72	16.9	1257	1	RBB1_HUMAN
10	66	15.5	429	1	DDPD2_MOUSE
11	65	15.3	443	1	HSLO_VIBCH
12	65	15.3	992	1	FLT3_MOUSE
13	65	15.3	1244	1	MIX1_CAEL
14	65	15.3	1388	1	RPDD_TORAC
15	65	15.3	1937	1	MYH8_HUMAN
16	64.5	15.1	335	1	UL25_HSV6Z
17	64	15.0	642	1	FLID_CAMJE
18	63.5	14.9	632	1	DNAX_ACTAC
19	63.5	14.9	1270	1	ITN1_XENLA
20	63	14.8	456	1	DDPD2_ARATH
21	62.5	14.7	205	1	KCUA_CHLPH
22	62.5	14.7	1658	1	ITN2_MOUSE
23	62	14.6	282	1	VIT4_CAEL
24	62	14.6	1033	1	V328_MYCPN
25	62	14.6	1041	1	DD16_HUMAN
26	62	14.6	1084	1	MYSS_RABIT
27	62	14.6	1935	1	MTSS_CYPCA
28	62	14.6	1938	1	MYH4_RABIT
29	62	14.6	1940	1	MYH3_CHICK
30	61.5	14.4	366	1	YE05_HAEIN
31	61.5	14.4	370	1	YA44_HELPY
32	61.5	14.4	378	1	UL25_HSV6G
33	61.5	14.4	555	1	UL25_HSV6U

34	61	14.3	910	1	HUL5_YEAST
35	61	14.3	1157	1	YE56_CAEL
36	60.5	14.2	707	1	RHO_SRLI
37	60.5	14.2	928	1	KINH_NEUCR
38	60.5	14.2	942	1	PKL1_HUMAN
39	60.5	14.2	1027	1	KINN_MOUSE
40	60.5	14.2	1032	1	KINN_HUMAN
41	60.5	14.2	1721	1	ITN1_HUMAN
42	60.5	14.2	1972	1	MYH8_HUMAN
43	60	14.1	455	1	MYH6_PSESS
44	60	14.1	465	1	MYH6_RABIT
45	60	14.1	1172	1	SVK2_MYCTU

ALIGNMENTS

RESULT 1	PTHY_HUMAN	STANDARD:	PRT:	115 AA.
ID	PTHY_HUMAN			
AC	P01270:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Parathyroid hormone precursor (Parathyrin) (PTH) (Parathormone).			
GN	PTH.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82150870: PubMed=6950381;			
RA	Hendy G.N., Kronenberg H.M., Potts J.T. Jr., Rich A.;			
RT	"Nucleotide sequence of cloned cDNAs encoding human preproparathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7365-7369(1981).			
RP	[2]			
RX	SEQUENCE FROM N.A.			
RA	MEDLINE=83169834: PubMed=6220408;			
RT	Vasilek T.J., McDevitt B.E., Freeman M.N., Fennick B.J.,			
RL	Hendy G.N., Potts J.T. Jr., Rich A., Kronenberg H.M.;			
RT	"Nucleotide sequence of the human parathyroid hormone gene."			
RL	Proc. Natl. Acad. Sci. U.S.A. 80:2127-2131(1983).			
RP	[3]			
RX	SEQUENCE OF 26-37.			
RA	MEDLINE=74174967: PubMed=4833516;			
RT	Jacobs J.W., Kemper B., Niall H.D., Habener J.F., Potts J.T. Jr.;			
RL	"Structural analysis of human parathyroid hormone by a new microsequencing approach."			
RL	Nature 249:155-157(1974).			
RP	[4]			
RX	SEQUENCE OF 32-68.			
RA	MEDLINE=74111656: PubMed=4521809;			
RT	Niall H.D., Sauer R.T., Jacobs J.W., Keutmann H.T., Segre G.V.,			
RL	O'Riordan J.L.H., Aurbach G.D., Potts J.T. Jr.;			
RT	"The amino-acid sequence of the amino-terminal 37 residues of human parathyroid hormone."			
RL	Proc. Natl. Acad. Sci. U.S.A. 71:384-388(1974).			
RP	[5]			
RX	SEQUENCE OF 61-83 AND 84-115.			
RA	MEDLINE=79082855: PubMed=728431;			
RT	Keutmann H.T., Sauer M.M., Hendy G.N., O'Riordan J.L.H.,			
RL	Potts J.T. Jr.;			
RT	"Complete amino acid sequence of human parathyroid hormone."			
RL	Biochemistry 17:5723-5729(1978).			
RP	[6]			
RX	SEQUENCE OF 75-100.			
RA	Keutmann H.T., Niall H.D., Jacobs J.W., Barling P.M., Hendy G.N.,			
RL	O'Riordan J.L.H., Potts J.T. Jr.;			
RT	(in) Talmadge R.V., Owen M., Parsons J.A. (eds.);			
RL	Calcium-regulating hormones, pp.9-14, Excerpta Medica Foundation,			
RL	Amsterdam (1975).			

```

CC      - - - - - send an email to license@elab-sib.ch) .
CC      DR      EMBL, J00301, AAA60215.1; -
CC      DR      EMBL, V00597, CAA23843.1; -
CC      DR      EMBL, A29146, CAA01956.1; -
CC      DR      PIR, A01536; PTH0.
CC      DR      PIR, A19339, A19339.
CC      DR      PDB, 1HPH: 10-JUL-95.
CC      DR      PDB, 1HTH: 15-OCT-97.
CC      DR      PDB, 1ZMA: 12-MAR-97.
CC      DR      PDB, 1ZMB: 12-MAR-97.
CC      DR      PDB, 1ZMB: 12-MAR-97.
CC      DR      PDB, 1ZME: 12-MAR-97.
CC      DR      PDB, 1ZWF: 16-JUN-97.
CC      DR      PDB, 1ZWG: 16-JUN-97.
CC      DR      PDB, 1BMX: 14-JAN-00.
CC      DR      PDB, 1HPY: 14-JAN-00.
CC      DR      Genew; HGNC:9606; PTH.
CC      DR      MIM, 146200; -.
CC      DR      InterPro: IPR001415; Parathyroid_hrm.
CC      DR      InterPro: IPR003625; pthythorm_sub.
CC      DR      Pfam, PF01279; Parathyroid_1.
CC      DR      ProDom, PD01687; pthythorm_sub; 1.
CC      DR      SMART, SM00087; PTH; 1.
CC      DR      PROSITE, PS00335; PARATHYROID; 1.
CC      KW      Hormone; Signal; Disease mutation; 3D-structure.
CC      FT      SIGNAL          1          25
CC      FT      PROPEP         26          31
CC      FT      CHAIN          32          115
CC      FT      VARIANT        18          18
CC      FT      CONFLICT       107          107
CC      FT      QUERY MATCH    115 AA; 12861 MM; 849015736465597 CAC64;
CC      FT      BEST LOCAL SIMILARITY 100.0%; Score 426; DB 1; Length 115;
CC      FT      MATCHES 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC      QY      1 SVSEIQLMHNNGKHLNSERVEMLKKKLIQDYVNFALGAPLAPRAGSOPRKKEKNVLY 60
CC      DB      32 SVSEIQLMHNNGKHLNSERVEMLKKKLIQDYVNFALGAPLAPRAGSOPRKKEKNVLY 91
CC      QY      61 ESHEKSLGEADKADYVNLTKAKSQ 84
CC      DB      92 ESHEKSLGEADKADYVNLTKAKSQ 115
CC      RESULT 2
CC      PTH_MACFA
CC      AC      O9XT35;
CC      DT      16-OCT-2001 (Rel. 40, Created)
CC      DT      16-OCT-2001 (Rel. 40, Last sequence update)
CC      DT      16-OCT-2001 (Rel. 40, Last annotation update)
CC      DE      Parathyroid hormone precursor (Parathyrin) (PTH).
CC      GN      PTH.
CC      OS      Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
CC      OC      Cercopithecinae; Macaca.
CC      OX      NCBI_TaxID=9541;
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A.
CC      RA      Malatiyitmond S., Takenaka O.;
CC      RT      "Nucleotide sequences of parathyroid gene in five species of macaque
CC      RT      of Thailand.";
CC      RL      J. Sci. Res. Chulalongkorn Univ. 23:135-142(1998).
CC      CC      -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL & DISSOLVING THE SALTS IN
CC      CC      BONE AND PREVENTING THEIR RECAL EXCRETION.
CC      CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: A130257; AAD42777.1; -;
DR HSSP: P01270; 1HPY.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.
DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SEQUENCE 115 AA; 12890 MW; 8C250DEF24BE597 CRC64;

Query Match 98.4%; Score 419; DB 1; Length 115;
Best Local Similarity 96.4%; Pred. No. 2.6e-39;
Matches 81; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIOLMHNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSORPRKEDNVLY 60
DB 32 SVSEIOLMHNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSORPRKEDNVLY 91
QY 61 ESHEKSLGEADKADVNLTKAKSQ 84
DB 92 ESHEKSLGEADKADVNLTKAKSQ 115

RESULT 3
PTHY_CANFA
ID PTHY_CANFA STANDARD; PRT; 115 AA.
AC P52212;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;

SEQUENCE FROM N.A.
RC TISSUE=Parathyroid;
RA Rosol T.J., Steimeyer C.L., McCauley L.K., Greene A.,
RA Demille J.W., Capen C.C.;
RT "Sequences of the cDNAs encoding canine parathyroid hormone-related
RT protein and parathyroid hormone.";
RT Gene 160:241-243(1995).
CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
CC BONE AND PREVENTING THEIR RENAL EXCRETION.
CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: U15662; AAA82584.1; -;
DR HSSP: P01268; 1ZWC.
DR InterPro: IPR001415; Parathyrd_hrm.
DR InterPro: IPR003625; Pthyrdorm_sub.

DR Pfam: PF01279; Parathyroid; 1.
DR ProDom: PD010687; Pthyrdorm_sub; 1.
DR SMART: SM00087; PTH; 1.
DR PROSITE: PS00335; PARATHYROID; 1.
DR Hormone; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT PROPEP 26 31 BY SIMILARITY.
FT CHAIN 32 115 PARATHYROID HORMONE.
SEQUENCE 115 AA; 12957 MW; FC38F77F1C8CFE56 CRC64;

Query Match 88.0%; Score 375; DB 1; Length 115;
Best Local Similarity 88.1%; Pred. No. 1.8e-34;
Matches 74; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 SVSEIOLMHNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSORPRKEDNVLY 60
DB 32 SVSEIOLMHNLGKHLNLSMERVEWLRKKLDVNFVALGAPLAPRDAGSORPRKEDNVLY 91
QY 61 ESHEKSLGEADKADVNLTKAKSQ 84
DB 92 ESHEKSLGEADKADVNLTKAKSQ 115

RESULT 4
PTHY_BOVIN
ID PTHY_BOVIN STANDARD; PRT; 115 AA.
AC P01268;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Parathyroid hormone precursor (Parathyrin) (PTH).
GN PTH.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;

SEQUENCE FROM N.A.
RA MEDLINE=8005617; PubMed=388425;
RA Kronenberg H.M., McDevitt B.E., Majzoub J.A., Nathan J., Sharp P.A.,
RA Potts J.T., Jr., Rich A.;
RT "Cloning and nucleotide sequence of DNA coding for bovine
RT preproparathyroid hormone.";
RT Proc. Natl. Acad. Sci. U.S.A. 76:4981-4985(1979).
[2]
SEQUENCE FROM N.A.
RA MEDLINE=82037785; PubMed=6170060;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Introduction by molecular cloning of artifactual inverted sequences
RT at the 5' terminus of the sense strand of bovine parathyroid hormone
RT cDNA.";
RT Proc. Natl. Acad. Sci. U.S.A. 78:4073-4077(1981).
[3]
SEQUENCE FROM N.A.
RA MEDLINE=83105964; PubMed=6185374;
RA Weaver C.A., Gordon D.F., Kemper B.;
RT "Nucleotide sequence of bovine parathyroid hormone messenger RNA.";
RT Mol. Cell. Endocrinol. 28:411-424(1982).
[4]
SEQUENCE FROM N.A.
RA MEDLINE=84262483; PubMed=6086460;
RA Weaver C.A., Gordon D.F., Kissil M.S., Mead D.A., Kemper B.;
RT "Isolation and complete nucleotide sequence of the gene for bovine
RT parathyroid hormone.";
RT Gene 28:319-329(1984).
[5]
SEQUENCE OF 26-115.
RA MEDLINE=74142666; PubMed=4522780;
RA Hamilton J.W., Miall H.D., Jacobs J.W., Keutmann H.T., Potts J.T., Jr.,
RA Cohn D.V.;
RT "The N-terminal amino-acid sequence of bovine parathyroid
RT hormone.";

Proc. Natl. Acad. Sci. U.S.A. 71:653-656(1974).

SEQUENCE OF 32-115.

MEDLINE-71076162; PubMed-5531031.

Nail H.D., Keutmann H.T., Sauer R., Hogan M.L., Dawson B.F.,
Aurbach G.D., Potts J.T. Jr.,
"The amino acid sequence of bovine parathyroid hormone I.",
Hoppe-Seyler's Z. Physiol. Chem. 351:1586-1588(1970).

SEQUENCE OF 32-115.

MEDLINE-71063634; PubMed-5275384;

Brewer H.B. Jr., Roman R.;
"Bovine parathyroid hormone: amino acid sequence.",
Proc. Natl. Acad. Sci. U.S.A. 67:1862-1869(1970).

SYNTHESIS OF 32-65.

MEDLINE-71091588; PubMed-4322265;

Potts J.T. Jr., Tregear G.W., Keutmann H.T., Nail H.D., Sauer R.,
Defeo L.J., Dawson B.F., Hogan M.L., Aurbach G.D.,
"Synthesis of a biologically active N-terminal tetraoctapeptide
of parathyroid hormone.",
Proc. Natl. Acad. Sci. U.S.A. 68:63-67(1971).

STRUCTURE BY NMR OF 32-68.

MEDLINE-20090619; PubMed-10623601;

Marx U.C., Ademann K., Bayer P., Forssmann W.-G., Rosch P.;
"Solution structures of human parathyroid hormone fragments
hPTH(1-34) and hPTH(1-39) and bovine parathyroid hormone fragment
bPTH(1-37).",
Biochem. Biophys. Res. Commun. 267:213-220(2000).

-1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.

-1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: V00106; CAA23439.1; -
EMBL: J00024; AAA30747.1; -
EMBL: K01938; AAA30749.1; -
EMBL: M25082; AAA30748.1; -
PIR: A01534; PTBO.
PIR: A24949; A24949.
PDB: 1ZWC; 12-MAR-97.
InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003625; Pthythorm_sub.
Pfam: PF01279; Parathyroid.1.
DR PRODOM: PD010687; Pthythorm_sub; 1.
DR SMART: SM00087; PTH.1.
DR PROSITE: PS00335; PARATHYROID.1.
KW Hormone; Signal; 3D-structure.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12960 MW; 2ED246B348880710 CRC64;

Query Match 85.7%; Score 365; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 2.2e-33;
Matches 72; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 SVSEIQLMHNKGLHNSREYEMLRKKIADYHNFAALGAPLAPDAGSORPRKKEDNVLY 60
DB 32 ASVEIQFMHNKGLHNSREYEMLRKKIADYHNFAALGASLAVRGGSSQRPKRKKEDNVLY 91

OY 61 ESHERSLGEADKADYVNLTKAKSQ 84
DB 92 ESHKSLGEADKADYVNLTKAKPQ 115

RESULT 5

PTHY_PIG STANDARD; PRT; 115 AA.

ID PTHY_PIG

AC P01269;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Parathyroid hormone precursor (Parathyrin) (PTH).

GN PTH.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

PN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-87316938; PubMed-3628009;

RA Schmelzer H.-J., Gross G., Widera G., Mayer H.;
"Nucleotide sequence of a full-length cDNA clone encoding
preparathyroid hormone from pig and rat.",
Nucleic Acids Res. 15:6740-6740(1987).

RL Nucleic Acids Res. 15:6740-6740(1987).

RN [2]

RP SEQUENCE OF 26-115.

RX MEDLINE-76018954; PubMed-1164500;

RA Chu L.H., Huang W.-Y., Littlelike E.T., Hamilton J.W., Cohn D.V.;
"Porcine preparathyroid hormone. Identification, biosynthesis, and
partial amino acid sequence.",
Biochemistry 14:3631-3635(1975).

RN [3]

RP SEQUENCE OF 32-115.

RX MEDLINE-7425317; PubMed-4840833;

RA Sauer R.T., Nail H.D., Hogan M.L., Keutmann H.T., O'Riordan J.L.H.,
Potts J.T. Jr.,
"The amino acid sequence of porcine parathyroid hormone.",
Biochemistry 13:1994-1999(1974).

RL Biochemistry 13:1994-1999(1974).

CC -1- FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.

CC -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL: X05722; CAA29193.1; -
PIR: A01535; PTPG.
PIR: B26806; B26806.
HSSP: P01270; 1BMX.
InterPro: IPR001415; Parathyrd_hrm.
InterPro: IPR003625; Pthythorm_sub.
Pfam: PF01279; Parathyroid.1.
DR PRODOM: PD010687; Pthythorm_sub; 1.
DR SMART: SM00087; PTH.1.
DR PROSITE: PS00335; PARATHYROID.1.
KW Hormone; Signal.
FT SIGNAL 1 25
FT PROPEP 26 31
FT CHAIN 32 115
FT CONFLICT 106 106 V -> G (IN REF. 4).
SQ SEQUENCE 115 AA; 12852 MW; 9FEB8CDEE14BAC16 CRC64;

Query Match 85.4%; Score 364; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 2.2e-33;
Matches 72; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 SVSEIQLMHNKGLHNSREYEMLRKKIADYHNFAALGAPLAPDAGSORPRKKEDNVLY 60
DB 32 ASVEIQFMHNKGLHNSREYEMLRKKIADYHNFAALGASLAVRGGSSQRPKRKKEDNVLY 91

OY 61 ESHERSLGEADKADYVNLTKAKSQ 84

```

DB      92 ESHKSLGEGADKADVLYLAKPQ 115

RESULT 6
PTHY_RAT STANDARD: PRT; 115 AA.
AC      P04089; 063473;
DT      01-NOV-1986 (Rel. 03, Created)
DT      01-NOV-1986 (Rel. 03, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Parathyroid hormone precursor (Parathyrin) (PTH).
GN      PTH.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
MEDLINE-84135846; PubMed-6321505;
Heinrich G., Kronenberg H.M., Potts J.T. Jr., Habener J.F.;
"Gene encoding parathyroid hormone. Nucleotide sequence of the rat
gene and deduced amino acid sequence of rat preproparathyroid
hormone.";
J. Biol. Chem. 259:3320-3329(1984).
RN      [2]
RP      SEQUENCE FROM N.A.
MEDLINE-87316938; PubMed-3628009;
Schmelzer H.-J., Gross G., Wildera G., Mayer H.;
"Nucleotide sequence of a full-length cDNA clone encoding
preproparathyroid hormone from pig and rat.";
Nucleic Acids Res. 15:6740-6740(1987).
RN      [3]
RP      SEQUENCE OF 10-115 FROM N.A.
TISSE-Parathyroid;
Schmelzer H.-J., Gross G., Mayer H.;
"Nucleotide sequence of cloned cDNA encoding rat prepro parathyroid
hormone.";
Adv. Gene Technol. 21:228-229(1984).
RN      [4]
RP      SEQUENCE OF 32-115 FROM N.A.
STRAIN-Sprague-Dawley; TISSE-Brain, Parathyroid, and Liver;
MEDLINE-96079910; PubMed-7388314;
Nutley M.T., Parlmi S.A., Harvey S.;
"Sequence analysis of hypothalamic parathyroid hormone messenger
ribonucleic acid.";
Endocrinology 136:5600-5607(1995).
RN      [5]
RP      FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: K01268; AAA41979.1; -
CC      EMBL: X05721; CA629192.1; -
CC      EMBL: M54875; AAA57156.1; -
CC      EMBL: S80127; -; NOT_ANNOTATED_CDS.
CC      PIR: A05091; A05091.
CC      PIR: A26806; A26806.
CC      HSSP: P01270; 12WB.
CC      InterPro: IPR001415; Parathyrd_hrm.
CC      InterPro: IPR003625; Pthythorm_sub.
CC      Pfam: PF01279; Parathyroid.1.
CC      ProDom: PD010687; pthythorm_sub; 1.
CC      SMART: SM00087; PTH; 1.
CC      ProSite: PS00335; PARATHYROID; 1.

```

```

KW      Hormone; Signal;
FT      SIGNAL 1 25
FT      PROPEP 26 31
FT      CHAIN 32 115
FT      CONFLICT 18 18
FT      CONFLICT 23 23
FT      CONFLICT 33 33
FT      CONFLICT 62 62
SQ      SEQUENCE 115 AA; 12722 MW; 7B434CFC528B230 CRC64;

Query Match
Best Local Similarity 74.4%; Score 317; DB 1; Length 115;
Matches 61; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY      1 SVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGARLAPRDAGSORPKKEDNVLV 60
DB      32 AVSEIOLMNLGKHLNLSMERVEWLRKKLDVNFVALGARLAPRDAGSORPKKEDNVLV 91
QY      61 ESHKSLGEGADKADVLYLAKSQ 84
DB      92 DGNKSLGEGADKADVLYLAKSQ 115

RESULT 7
PTHY_CHICK STANDARD: PRT; 119 AA.
AC      P15743;
DT      01-APR-1990 (Rel. 14, Created)
DT      01-APR-1990 (Rel. 14, Last sequence update)
DT      15-JUL-1998 (Rel. 36, Last annotation update)
DE      Parathyroid hormone precursor (PTH).
OC      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
MEDLINE-89219100; PubMed-2710135;
Russell J., Sherwood L.M.;
"Nucleotide sequence of the DNA complementary to avian (chicken)
preproparathyroid hormone mRNA and the deduced sequence of the
hormone precursor.";
Mol. Endocrinol. 3:325-331(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
MEDLINE-89284968; PubMed-3251402;
Khosla S., Demay M., Pines M., Hurwitz S., Potts J.T. Jr.,
Kronenberg H.M.;
"Nucleotide sequence of cloned cDNAs encoding chicken
preproparathyroid hormone.";
J. Bone Miner. Res. 3:689-698(1988).
RN      [3]
RP      FUNCTION: PTH ELEVATES CALCIUM LEVEL BY DISSOLVING THE SALTS IN
BONE AND PREVENTING THEIR RENAL EXCRETION.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      -1- SIMILARITY: BELONGS TO THE PARATHYROID HORMONE FAMILY.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: M31604; AAA49093.1; -
CC      EMBL: M36522; AAB02866.1; -
CC      PIR: A34937; A34937.
CC      HSSP: P01270; 1HPY.
CC      InterPro: IPR001415; Parathyrd_hrm.
CC      InterPro: IPR003625; Pthythorm_sub.
CC      Pfam: PF01279; Parathyroid.1.
CC      ProDom: PD010687; pthythorm_sub; 1.
CC      SMART: SM00087; PTH; 1.

```

DR PROSITE: PS00335; PARATHYROID. 1.
 KW Hormone; Signal. 1.
 FT SIGNAL 1 25
 FT PROPEP 26 31
 FT CHAIN 32 119
 SQ SEQUENCE 119 AA; 13943 MW; B309DBE772997FEE CRC64;
 Query Match
 Best Local Similarity 43.18; Score 183.5; DB 1; Length 119;
 Matches 44; Conservative 13; Mismatches 17; Indels 21; Gaps 2;
 QY 1 SVSEIQLNHNKGLNSRVEVLRKKLDVHNFAALGAPLPAPRAGSORPKKEDNVLY 60
 DB 32 SVSEIQLNHNKGLNSRVEVLRKKLDVHNFAALGAPLPAPRAGSORPKKEDNVLY 60
 QY 61 E-----SHEKSLGEADKADVNVLTAK 82
 DB 84 EIRNRLLPEHLRAAVOKKSIDLKAVNVVLFKTK 118
 RESULT 8
 ID STYL_THEME STANDARD; PRT; 824 AA.
 AC Q9WY15;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (Leurs).
 GN LEUS OR TM0168.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogae; Thermotogales;
 OC Thermotogaceae; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MS8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Elsen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 genome sequence of Thermotoga maritima.";
 RL Nature 399:323-329(1999).
 CC -1- CATALYTIC ACTIVITY: ATP + L-Leucine + tRNA(Leu) = AMP +
 diphosphate + L-leucyl-tRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AE001702; AAD35261.1;
 DR TIGR: TM0168;
 DR InterPro: IPR002302; Leu-tRNA synthetase.
 DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00133; tRNA-synt_1.1.
 DR PRINTS: PRO0095; TRNASYNTHLEU.
 DR TIGR: TIGR00396; LeuS_bact.1.
 DR PROSITE: PS00178; AA-tRNA ligase; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 41 51 "HIGH" REGION.
 FT SITE 580 584 "TMSKS" REGION.
 FT BINDING 583 583 ATP (BY SIMILARITY).

SQ SEQUENCE 824 AA; 95624 MW; 7CB0252A76A844EC CRC64;
 Query Match
 Best Local Similarity 23.38; Score 74.5; DB 1; Length 824;
 Matches 21; Conservative 26; Mismatches 24; Indels 19; Gaps 4;
 QY 5 IQLNHNKGLNSRVEVLRKKLDVHNFAALGAPLPAPRAGSORPKKEDNVLY 60
 DB 692 MELVNHLSQYLSNVSPQGEVNRKKLRLEIVKLTALSFAPHLAEFVHDLGN-----D 744
 QY 57 NVLVE-----SHEKSLGEADKADVNVLTAK 82
 DB 745 SLVYQOSWSPYDPKALVEVEEVAIQNGK 774
 RESULT 9
 ID RBBI_HUMAN STANDARD; PRT; 1257 AA.
 AC P29374; Q15991; Q15992; Q15993;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Retinoblastoma-binding protein 1 (RBBP-1).
 GN RBBP1 OR RBPI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM I).
 RC MEDLINE=94020841; PubMed=8414517;
 RA Fattley A.R., Helin K., Dembski M.S., Dyson N., Harlow E.,
 RA Vuocolo G.A., Hanblik M.G., Haskell K.M., Olfiff A., Defeo-Jones D.,
 RA Jones R.E.;
 RT "Characterization of the retinoblastoma binding proteins RBP1 and
 RBP2.";
 RL Oncogene 8:3149-3156(1993).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND ALTERNATIVE SPLICING.
 RC MEDLINE=93205410; PubMed=8455946;
 RA Otterson G.A., Klatze R.A., Lin A.Y., Johnston P.G., Kaye F.J.;
 RT "Alternative splicing of the RBP1 gene clusters in an internal exon
 RT that encodes potential phosphorylation sites.";
 RL Oncogene 8:949-957(1993).
 RN [3]
 RP SEQUENCE OF 855-1203 FROM N.A. (ISOFORM I).
 RC MEDLINE=91312450; PubMed=1857421;
 RA Defeo-Jones D., Huang P.S., Jones R.E., Haskell K.M., Vuocolo G.A.,
 RA Hanblik M.G., Huber H.E., Olfiff A.;
 RT "Cloning of cDNAs for cellular proteins that bind to the
 RT retinoblastoma gene product.";
 RL Nature 352:251-254(1991).
 CC -1- FUNCTION: INTERACTS WITH THE VIRAL PROTEIN-BINDING DOMAIN OF THE
 CC RETINOBLASTOMA PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; I (shown here), II and III; are
 CC produced by alternative splicing.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: S66427; AAB28543.1;
 DR EMBL: S57153; AAB25833.1;
 DR EMBL: S57160; AAB25834.1;
 DR EMBL: S57162; AAB25835.2;
 DR FTR: S16953; S16953.
 DR Genew: HGNC:9885; RBBP1.
 DR MIM: 180201;

DR InterPro: IPR001606; ARID.
 DR InterPro: IPR000953; Chromo.
 DR InterPro: IPR002999; Tudor.
 DR Pfam: PF01388; ARID; 1.
 DR SMART: SM00501; BRIGANT; 1.
 DR SMART: SM00298; CHROMO; 1.
 DR SMART: SM00333; TUDOR; 1.
 KM Trans-acting factor; Nuclear protein; Alternative splicing.
 FT DOMAIN 951 964
 FT RETINOBLASTOMA PROTEIN BINDING
 FT (POTENTIAL).
 FT VARSPIC 1106 1174 MISSING (IN ISOFORM III).
 FT VARSPIC 1175 1175 N -> D (IN ISOFORM III).
 FT VARSPIC 1121 1174 MISSING (IN ISOFORM II).
 FT CONFLICT 385 385 L -> V (IN REF. 2).
 FT CONFLICT 618 618 S -> R (IN REF. 2).
 FT CONFLICT 653 653 K -> V (IN REF. 2).
 FT CONFLICT 779 779 A -> T (IN REF. 2).
 FT CONFLICT 1178 1178 D -> S (IN REF. 3).
 FT CONFLICT 1196 1201 IRKYVM -> SEITICL (IN REF. 3).
 FT SEQUENCE 1257 AA; 142666 MW; F3C0ABD6DE43DC CRC64;

Query Match 16.9%; Score 72; DB 1; Length 1257;
 Best Local Similarity 26.8%; Pred. No. 5.9;
 Matches 19; Conservative 21; Mismatches 27; Indels 4; Gaps 2;

QY 14 HUNSMERVELARKKODVHN-FVALGAPLAPRAGSQRPRKEDNVLVESHERSLGEADK 72
 DB 1179 NMSTIRISLQKLEIRKYVMSKSEVATIDRRRLKDKREV---SHAGSMSSAS 1235

QY 73 ADVNVLTKAKS 83
 DB 1236 SDGMSPPSSS 1246

RESULT 10
 ID DP2.ORYSA STANDARD; PRT; 429 AA.
 AC 09LRES; 09SNL2; 40. Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE DNA polymerase delta small subunit (EC 2.7.7.7).
 GN POL2
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 [1]
 SEQUENCE FROM N.A.
 RA Hatanaka M., Kimura S., Sakaguti K.;
 RT "Oryza sativa DNA polymerase delta small subunit."
 RN Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Saeki T., Matsunoto T., Yamamoto K.;
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: THE FUNCTION OF THE SMALL SUBUNIT IS NOT YET CLEAR.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
 + (DNA)(N).
 CC -1- SUBUNIT: HETERODIMER WITH SUBUNITS OF 125 KDA AND 50 KDA (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE DNA POLYMERASE DELTA/II SMALL SUBUNIT
 FAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch.
 CC -----
 DR EMBL: AB037900; BAA99574.1; -
 DR EMBL: AP000615; BAA85393.1; -
 KM Transferrase; DNA-directed DNA polymerase; DNA replication;
 KM Nuclear protein.
 FT CONFLICT 256 256 Q -> QVS (IN REF. 2).
 FT CONFLICT 411 414 LMLR -> VNTSCHLTGKALFYIC (IN REF. 2).
 FT CONFLICT 418 429 CSTLSPTSFDA -> SYKEAKSSGD (IN REF. 2).
 SO SEQUENCE 429 AA; 48000 MW; 10BA6ED519EBB67 CRC64;

Query Match 15.5%; Score 66; DB 1; Length 429;
 Best Local Similarity 28.4%; Pred. No. 7.6;
 Matches 23; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY 6 QLMHNIGKHSNEREMRLKRDVHNVALGAPLAPRAGSQRPRKEDNVLVES--H 63
 DB 318 QNIDDLTKYSDAKDKLEFVEFRLMRHL-----APAPNSLQCY-PYTDKDFLVESCPH 371

QY 64 EKSLGEADKADVNVLTAKSQ 84
 DB 372 VYFVGNDKYEFGQLGLEKQ 392

RESULT 11
 ID HSLU_VIBCH STANDARD; PRT; 443 AA.
 AC 09KN07;
 DT 16-OCT-2001 (Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE ATP-dependent hsl protease ATP-binding subunit hslu.
 GN HSLU OR VC2674.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 NCBI_TaxID=66;
 [1]
 SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 cholerae."
 RT Nature 406:477-483(2000).
 CC -1- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
 COMPLEX (BY SIMILARITY).
 CC -1- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.

 This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation
 at the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>)
 or send an email to license@isb-sib.ch.

 EMBL: AE004333; AAP5815.1; -
 DR HSPB; P32168; ID02.
 DR TIGR; VC2674; -
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003959; AAA_ATPase_centre.
 DR InterPro: IPR004491; Hsp_HsluV.
 DR Pfam: PF00004; AAA; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMs: TIGR00390; Hslu; 1.

KW Chapterone: ATP-binding: Complete proteome.
 FT NP_BIND 57 64 ATP (POTENTIAL).
 SQ SEQUENCE 443 AA; 49900 MW; DAEL3E82FAB6A38F CRC64;
 Query Match 15.3%; Score 65; DB 1; Length 443;
 Best Local Similarity 29.7%; Pred. No. 10;
 Matches 19; Conservative 13; Mismatches 30; Indels 2; Gaps 1;
 QY 14 HLNSEMEVRLRKKLQDVHVALGAPLAPRAGSQPRKEDNVLVESHEKSLGEADKA 73
 DB 112 HQQMEKVFRAEELAEERVLDALEPP--PRDAGQAEQKENSSTQVFRKKURECOLN 169
 QY 74 DVNV 77
 DB 170 DKEL 173
 RESULT 12
 FLT3_MOUSE STANDARD; PRT; 992 AA.
 ID FLT3_MOUSE 000342;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FL cytokine receptor precursor (EC 2.7.1.112) (tyrosine-protein kinase receptor flk-2) (fetal liver kinase 2) (tyrosine-protein kinase FLT3).
 GN FLT3 OR FLT-3 OR FLK-2.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91292518; PubMed=1648448;
 RA Matthews W., Jordan C.T., Miegand G.W., Pardoll D., Lemischka I.R.;
 RT "A receptor tyrosine kinase specific to hematopoietic stem and progenitor cell-enriched populations.";
 RL Cell 65:1143-1152(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92019834; PubMed=1656368;
 RA Rosnet O., Marchetto S., Delapeyriere O., Birnbaum D.;
 RT "Murine Flt3, a gene encoding a novel tyrosine kinase receptor of the PDGFR/CSF1R family.";
 RL Oncogene 6:1641-1650(1991).
 RN [3]
 RP CHARACTERIZATION.
 MEDLINE=93203405; PubMed=8384358;
 RA Marot N., Rottapel R., Rosnet O., Marchetto S., Lavezzl C., Mannoni P., Birnbaum D., Dubreuil P.;
 RT "Biochemical characterization and analysis of the transforming potential of the FLT3/FLK2 receptor tyrosine kinase.";
 RL Oncogene 8:909-918(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE FL CYTOKINE. HAS A TYROSINE-PROTEIN KINASE ACTIVITY.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: HEMATOPOIETIC STEM AND PROGENITOR CELL-ENRICHED POPULATIONS. FOUND IN BRAIN, PLACENTA AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-PROTEIN KINASES.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation- the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC

DR EMBL: M64689; AAA37634.1; -;
 DR EMBL: X59398; CAA42041.1; -;
 DR PIR: A39931; A39931.
 DR HSSP: P11362; IFGK.
 DR MGD: MGT:95559; FLT3.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR001824; RTkinaseII.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Ig_1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 2.
 DR SMART: SM00410; Ig_Like; 1.
 DR SMART: SM00219; TYRC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00240; RECEPTOR_TYR_KIN_ITI; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Signal: Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 KW Glycoprotein; Phosphorylation; ATP-binding; Immunoglobulin domain.
 FT SIGNAL 1 27
 FT CHAIN 28 992
 FT DOMAIN 28 544
 FT TRANSMEM 545 564
 FT DOMAIN 565 992
 FT DOMAIN 611 946
 FT NP_BIND 617 625
 FT BINDING 645 645
 FT ACT_SITE 814 814
 FT CARBOHYD 44 44
 FT CARBOHYD 133 133
 FT CARBOHYD 152 152
 FT CARBOHYD 307 307
 FT CARBOHYD 324 324
 FT CARBOHYD 352 352
 FT CARBOHYD 445 445
 FT CARBOHYD 474 474
 FT CARBOHYD 503 503
 FT CARBOHYD 542 542
 FT CONFLICT 150 150
 FT CONFLICT 242 242
 FT CONFLICT 726 726
 FT CONFLICT 957 979
 FT CONFLICT 983 983
 SQ SEQUENCE 992 AA; 112639 MW; 407A08785372100 CRC64;
 Query Match 15.3%; Score 65; DB 1; Length 992;
 Best Local Similarity 21.7%; Pred. No. 26;
 Matches 28; Conservative 17; Mismatches 32; Indels 52; Gaps 4;
 QY 2 VSEIQMLNHLGKHLNM-----ERYEWLKKLQDV----- 31
 DB 660 MSELKMTHTLGHNDIVNLGACTLSGPVYLIFECYCDYDLNLTKSKREKFRHTWTEIF 719
 QY 32 --HNF-----VALGAPLAPRAGSQPRKEDNVLVESHEKSLGEA 70
 DB 720 KEHNSSYTFQAHNSNMPGSRREVOLHPDQLQSGFNNSIHSEDEIYE--NOKRLAE 778
 QY 71 DRADVAVLT 79
 DB 779 EEDDLNVL 787
 RESULT 13
 MIXI_CAEEL STANDARD; PRT; 1244 AA.
 ID MIXI_CAEEL 009591;
 AC 009591;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitotic chromosome and X-chromosome associated protein mix-1.


```

GN      MIX-1 OR M106.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxId=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98117254; PubMed=9458050;
RA      Lieb J.D., Albrecht M.R., Chuang P.T., Meyer B.J.;
RT      "M1-1: an essential component of the C. elegans mitotic machinery
RT      executes x chromosome dosage compensation."
RN      Cell 92:265-277(1998).
[2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Bristol N2;
RA      Palmer S.;
CC      Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC      -1- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
CC      PLANKED BY PUTATIVE GLOBAL REGIONS AT THE N- AND C-TERMINUS.
CC      -1- SIMILARITY: BELONGS TO THE SMC FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC      The European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; U96387; AAC47834.1;
DR      EMBL; 246935; CAA87054.1;
DR      EMBL; AL031266; CAA20330.1;
DR      EMBL; 246794; CAA20330.1; JOINED.
DR      EMBL; 246935; CAA20330.1; JOINED.
DR      EMBL; 246794; CAA86786.1;
DR      EMBL; AL031266; CAA86786.1; JOINED.
DR      EMBL; 246935; CAA86786.1; JOINED.
DR      Wormpep: M106.1; CE18083.
DR      InterPro: IPR003405; SMC_C.
DR      InterPro: IPR003195; SMC_N.
DR      Pfam: PF02463; SMC_N; 1.
DR      Pfam: PF02483; SMC_C; 1.
DR      Pfam: PD00006; ABC transporter; 1.
DR      ATP-binding; Coiled coil; Nuclear protein.
NP_BIND
NP_BIND 32 39
FT      DOMAIN 245 350 COILED COIL (POTENTIAL).
FT      DOMAIN 415 479 COILED COIL (POTENTIAL).
FT      DOMAIN 702 1043 COILED COIL (POTENTIAL).
FT      DOMAIN 1109 1135 ALA/ASP-RICH (DA-BOX).
FT      DOMAIN 1239 1242 POLY-ASP.
SQ      SEQUENCE 1244 AA; 140341 MW; 255FD9C3DBC4AA49 CRC64;

Query Match 15.3%; Score 65; DB 1; Length 1244;
Best Local Similarity 26.8%; Pred. No. 34;
Matches 22; Conservative 16; Mismatches 34; Indels 10; Gaps 2;

OY 7 LMHNIGKILNSER-----VENIRKKLVYHNHFVALGAPLAPRDAGSQRP RKEDNVYES 62
Db 756 VVRDLKVSSEEEKQAEIEATVTKLKDVEDKIKITLESNMKNKDSQERKKELTALLQK 815
OY 63 HE-----KSLGEADKADVNVL 78
Db 816 AEQTYAKNKNRGEKARREVMIL 837

RESULT 14
RPOD_TOBAC STANDARD: PRT: 1388 AA.
ID RPOD_TOBAC

```

```

AC      P38550.1 01-OCT-1994 (Rel. 30. Created)
AD      01-OCT-1994 (Rel. 30. Last sequence update)
AE      16-OCT-2001 (Rel. 40. Last annotation update)
AF      DNA-directed RNA polymerase beta' chain (EC 2.7.7.6).
AG      RPOC2.
AH      Nicotiana tabacum (Common tobacco).
AI      Chloroplast.
AJ      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AK      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
AL      Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
AM      NCBI_TaxID=4097;
AN      [1]
AO      SEQUENCE FROM N.A.
AP      STRAIN=cv. Bright yellow 4;
AQ      Shirozaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
AR      Matsubayashi T., Zalta N., Chunwongse J., Oookata J.,
AS      Yamaguchi-Shinozaki K., Ohio C., Torazawa K., Meng B.-Y., Sugita M.,
AT      Deno H., Kamogashira T., Yamada K., Kinsuda J., Takaiwa F., Kato A.,
AU      Tohoh N., Shimada H., Sugitara M.;
AV      "The complete nucleotide sequence of the tobacco chloroplast genome:
AW      its gene organization and expression.";
AX      EMBO J. 5:2043-2049(1986).
AY      [2]
AZ      REVISONS.
BA      MEDLINE=94003079; PubMed=8400137;
BB      Olmstead R.G., Sweere J.A., Wolfe K.H.;
BC      "Ninety extra nucleotide in ndhF gene of tobacco chloroplast DNA: a
BD      summary of revisions to the 1986 genome sequence.";
BE      Plant Mol. Biol. 22:1191-1193(1993).
BF      -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
BG      OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
BH      SUBSTRATES.
BI      -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
BJ      {RNA}(N).
BK      -!- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
BL      SUBUNITS: ALPHA, BETA, BETA', AND BETA".
BM      -----
BN      This SWISS-PROT entry is copyright. It is produced through a collaboration
BO      between the Swiss Institute of Bioinformatics and the EMBL outstation
BP      at the European Bioinformatics Institute. There are no restrictions on
BQ      use by non-profit institutions as long as its content is in no way
BR      modified and this statement is not removed. Usage by and for commercial
BS      entities requires a license agreement (See http://www.isb-sdb.ch/announce
BT      or send an email to license@isb-sdb.ch).
BU      -----
BV      EMBL: Z00044; CAA77410.1; ALT_SEQ.
BX      HSSP: O9KW06; IHOM.
BY      InterPro: IPR000722; RNA_pol_A.
BZ      InterPro: IPR002879; RNA_pol_A2.
CA      Pfam: PF00623; RNA_pol_A; 1.
CB      Pfam: PF01854; RNA_pol_A2; 2.
CC      Transference: Transcription; DNA-directed RNA polymerase; Chloroplast.
CD      SEQUENCE 1388 AA; 156840 MW; 41FD7F238913188C CRC64;
CE
CF
CG
CH
CI
CJ
CK
CL
CM
CN
CO
CP
CQ
CR
CS
CT
CU
CV
CW
CX
CY
CZ
DA
DB
DC
DD
DE
DF
DG
DH
DI
DJ
DK
DL
DM
DN
DO
DP
DQ
DR
DS
DT
DU
DV
DW
DX
DY
DZ
EA
EB
EC
ED
EE
EF
EG
EH
EI
EJ
EK
EL
EM
EN
EO
EP
EQ
ER
ES
ET
EU
EV
EW
EX
EY
EZ
FA
FB
FC
FD
FE
FF
FG
FH
FI
FJ
FK
FL
FM
FN
FO
FP
FQ
FR
FS
FT
FU
FV
FW
FX
FY
FZ
GA
GB
GC
GD
GE
GF
GG
GH
GI
GJ
GK
GL
GM
GN
GO
GP
GQ
GR
GS
GT
GU
GV
GW
GX
GY
GZ
HA
HB
HC
HD
HE
HF
HG
HH
HI
HJ
HK
HL
HM
HN
HO
HP
HQ
HR
HS
HT
HU
HV
HW
HX
HY
HZ
IA
IB
IC
ID
IE
IF
IG
IH
II
IJ
IK
IL
IM
IN
IO
IP
IQ
IR
IS
IT
IU
IV
IW
IX
IY
IZ
JA
JB
JC
JD
JE
JF
JG
JH
JI
JJ
JK
JL
JM
JN
JO
JP
JQ
JR
JS
JT
JU
JV
JW
JX
JY
JZ
KA
KB
KC
KD
KE
KF
KG
KH
KI
KJ
KK
KL
KM
KN
KO
KP
KQ
KR
KS
KT
KU
KV
KW
KX
KY
KZ
LA
LB
LC
LD
LE
LF
LG
LH
LI
LJ
LK
LM
LN
LO
LP
LQ
LR
LS
LT
LU
LV
LW
LX
LY
LZ
MA
MB
MC
MD
ME
MF
MG
MH
MI
MJ
MK
ML
MN
MO
MP
MQ
MR
MS
MT
MU
MV
MW
MX
MY
MZ
NA
NB
NC
ND
NE
NF
NG
NH
NI
NJ
NK
NL
NM
NO
NP
NQ
NR
NS
NT
NU
NV
NW
NX
NY
NZ
OA
OB
OC
OD
OE
OF
OG
OH
OI
OJ
OK
OL
OM
ON
OO
OP
OQ
OR
OS
OT
OU
OV
OW
OX
OY
OZ
PA
PB
PC
PD
PE
PF
PG
PH
PI
PJ
PK
PL
PM
PN
PO
PP
PQ
PR
PS
PT
PU
PV
PW
PX
PY
PZ
QA
QB
QC
QD
QE
QF
QG
QH
QI
QJ
QK
QL
QM
QN
QO
QP
QQ
QR
QS
QT
QU
QV
QW
QX
QY
QZ
RA
RB
RC
RD
RE
RF
RG
RH
RI
RJ
RK
RL
RM
RN
RO
RP
RS
RT
RU
RV
RW
RX
RY
RZ
SA
SB
SC
SD
SE
SF
SG
SH
SI
SJ
SK
SL
SM
SN
SO
SP
SQ
SR
SS
ST
SU
SV
SW
SX
SY
SZ
TA
TB
TC
TD
TE
TF
TG
TH
TI
TJ
TK
TL
TM
TN
TO
TP
TQ
TR
TS
TT
TU
TV
TW
TX
TY
TZ
UA
UB
UC
UD
UE
UF
UG
UH
UI
UJ
UK
UL
UM
UN
UO
UP
UQ
UR
US
UT
UU
UV
UW
UX
UY
UZ
VA
VB
VC
VD
VE
VF
VG
VH
VI
VJ
VK
VL
VM
VN
VO
VP
VQ
VR
VS
VT
VU
VV
VW
VX
VY
VZ
WA
WB
WC
WD
WE
WF
WG
WH
WI
WJ
WK
WL
WM
WN
WO
WP
WQ
WR
WS
WT
WU
WV
WW
WX
WY
WZ
XA
XB
XC
XD
XE
XF
XG
XH
XI
XJ
XK
XL
XM
XN
XO
XP
XQ
XR
XS
XT
XU
XV
XW
XX
XY
XZ
YA
YB
YC
YD
YE
YF
YG
YH
YI
YJ
YK
YL
YM
YN
YO
YP
YQ
YR
YS
YT
YU
YV
YW
YX
YY
YZ
ZA
ZB
ZC
ZD
ZE
ZF
ZG
ZH
ZI
ZJ
ZK
ZL
ZM
ZN
ZO
ZP
ZQ
ZR
ZS
ZT
ZU
ZV
ZW
ZX
ZY
ZZ

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=90333631; PubMed=2373371;
 RA Karsch-Mizrachi I., Feghali R., Shows T.B. Jr., Lelwand L.A.;
 RT "Generation of a full-length human perinatal myosin heavy-chain-
 encoding cDNA";
 RL Gene 89:289-294(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=95324556; PubMed=7601129;
 RA Jullian E.H., Kelly A.M., Pompidou A.J., Hoffman R., Schiaffino S.,
 RA Steadman H.H., Rubinstein N.A.;
 RT "Characterization of a human perinatal myosin heavy-chain
 transcript.";
 RL Eur. J. Biochem. 230:1001-1006(1995).
 RN [3]
 RP SEQUENCE OF 507-1937 FROM N.A.
 RC TISSUE-Skeletal muscle;
 RX MEDLINE=90233862; PubMed=1691980;
 RA Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
 RA Arnold H.H.;
 RT "Identification of three developmentally controlled isoforms of human
 myosin heavy chains";
 RL Eur. J. Biochem. 189:55-65(1990).
 RN [4]
 RP SEQUENCE OF 860-1937 FROM N.A.
 RX MEDLINE=89234168; PubMed=2715179;
 RA Feghali R., Lelwand L.A.;
 RT "Molecular genetic characterization of a developmentally regulated
 human perinatal myosin heavy chain";
 RL J. Cell Biol. 108:1791-1797(1989).
 RN [5]
 RP SEQUENCE OF 1-46 FROM N.A.
 RA Esser K., Tichar A., Myszkowski M.;
 RT "Isolation and characterization of the human perinatal MHC promoter";
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: MUSCLE CONTRACTION.
 CC -1- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2
 CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
 CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
 CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
 CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
 CC CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
 CC -1- PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY
 CC ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
 CC -1- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
 CC MEROMYOSIN (LM) AND 1 HEAVY MEROMYOSIN (HM). IT CAN LATER BE
 CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
 CC SUBFRAGMENT (S2).
 CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IQ DOMAIN.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use. By non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: M36769; AAC17185.1;
 CC EMBL: Z38133; CA86293.1;
 CC EMBL: X51592; CA35941.1;
 CC EMBL: AF067143; AAC21557.1;
 CC PIR: A30220; A30220.
 CC HSP: P13538; ZMYS.

DR Genew; HGNC:7578; MYH8.
 DR MIM: 160741;
 DR InterPro: IPR0000048; IQ_region.
 DR InterPro: IPR004009; Myosin_N.
 DR InterPro: IPR002928; Myosin_tail.
 DR InterPro: IPR001609; myosin_head.
 DR Pfam: PF00063; myosin_head.
 DR Pfam: PF00612; IQ_1.
 DR Pfam: PF01576; Myosin_tail; 1.
 DR Pfam: PF02736; Myosin_N; 1.
 DR PRINTS: PR00193; MYOSINHEAVY.
 DR ProDom: PD000355; myosin_head; 1.
 DR SMART: SM00242; MYSC; 1.
 DR SMART: PS50096; IQ; 1.
 DR PROSITE: PS50096; IQ; 1.
 DR Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding;
 DR ATP-binding; Methylation; Alkylation; Multigene family;
 DR Calmodulin-binding.
 DR MYOSIN HEAD-LIKE.
 DR IQ.
 DR COILED COIL (POTENTIAL).
 DR ATP.
 DR ACTIN-BINDING.
 DR ACTIN-BINDING.
 DR METHYLATION (SH-1) (POTENTIAL).
 DR ALKYLATION (SH-2) (POTENTIAL).
 DR ALKYLATION (SH-1) (POTENTIAL).
 DR A -> R (IN REF. 2).
 DR E -> Q (IN REF. 1 AND 4).
 DR M -> N (IN REF. 3).
 DR N -> H (IN REF. 1 AND 4).
 DR MC -> DGG (IN REF. 3).
 DR E -> G (IN REF. 1 AND 4).
 DR K -> Q (IN REF. 1 AND 4).
 DR KY -> NT (IN REF. 3).
 DR EN -> AH (IN REF. 1 AND 4).
 DR E -> D (IN REF. 1 AND 4).
 DR D -> H (IN REF. 2).
 DR SQ SEQUENCE 1937 AA; 222762 MW; A3EE2D151792E9E8 CRC64;

Query Match 15.3%; Score 65; DB 1; Length 1937;
 Best Local Similarity 42.4%; Pred. NO. 58;
 Matches 14; Conservative 10; Mismatches 7; Indels 2; Gaps 1;
 QY 54 KEDNTLVESHESLG--EADKADVAVLTKAKSQ 84
 DB 997 KKKALQETHOOTLDLQAEEDKVNILTKAKTK 1029

Search completed: November 21, 2002, 17:13:08
 Job time : 17.6154 secs